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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

July 10, 2004, 07:02:02; Search time 147 Seconds (without alignments) 7614.530 Million cell updates/sec Run on:

US-09-813-492-1 2017

Perfect score: Sequence:

682709 seqs, 277475446 residues Searched:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*
5: /cgn2\_6/ptodata/2/ina/PcTUS\_COMB.seq:\*
6: /cgn2\_6/ptodata/2/ina/PcTUS\_COMB.seq:\* Issued Patents NA:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Seminary A contained		Semience 7 Appli		, , ,	Sequence 3. Appli		Ì	Sequence 16. Annl		ì	Semience 1. Appli	ì	10	1 4 0	32	3 15	967	-	Sequence 1. Appli	· ~	· ~	, ,	1 ~	- 0	0 0	
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	Query	51.3	23.6	18.8	15.0	11.4	11.1	11.1	10.9	10.9	10.9	10.9	10.8	10.8	10.8	10.8	10.7	10.7	10.7	10.7	10.7	10.6	10.6	10.6	10.6	10.6	10.6	10.6
	Score	1035.2	475.6	379	302	230	224	223.6	220.4	220.2	220.2	219.2	218.6	218.2	217.4		216.8	216.4	216.4	216.4	216.4	214.8	214.6	214.4	214.4	214.4	213.6	213.2
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Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 79, Appli Sequence 79, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 1, Appli	63,
US-09-984-880-3 US-10-277-032-3 US-09-916-204-3 US-09-044-471A-3 US-09-618-1891-79 US-09-6718-16-79 US-09-404-879A-1 US-09-404-879A-3 US-09-338-933-3 US-09-338-933-3 US-09-215-681-3 US-09-215-681-3 US-09-216-003A-1 US-09-216-003A-1 US-09-216-003A-1 US-09-216-003A-1 US-09-216-003A-1 US-09-216-003A-1 US-09-216-003A-1 US-09-216-003A-1 US-09-216-003A-1	US-09-340-620A-63
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## ALIGNMENTS

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Sequence 6, Application US/09146580A
| Patent No. 6306653
| Fatent No. 6306653
| Patent No. 630659
| Patent No. 630691
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FEATURE:
NAME/KEY: unsure
LOCATION: (35)
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OTHER INFORMATION: N
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US-09-146-580-6
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0 Ö Length 3117; DB 4; 51.3%; Score 1035.2; Query Match

15;	730	1728	790	1788	850	1848	910	1908
Best Local Similarity 86.5%; Pred. No. 1.2e-228; Matches 1172; Conservative 73; Mismatches 92; Indels 18; Gaps	671 GGTATGCAAATGTAGCCAATAATATCTCAAAGCTCCAGGGCTCAAGCGATCCTCCCACCT	1669 GGTCTCACTATGTTGCCCAGGTTGATCTCAAACTCCTGGGCTCAAGCGATCCTCCCACCT 1728	731 TAGCCTCCCAAAGTACTGGGATTATAGGTGTGAGCCACAGTGCCTGGCCTAATTATTTC 790	1729 TAGCCTCCCAAAGTACTGGGATTATAGGTGTGAGCCACAGTGCCTGGCCTAATTATTTC 1788	791 ITGTGATCAAATTCAGGTTTAATGTTTTTGGTTAAGAATTTCCTACGTGAATTCCTGTAC 850	1789 TIGTGATCAAATTCAGGTTTAATGTTTTTGGTTAAGAATTTCCTACGTGAATTGGTGTAC 1848	851 TTATTTTGTCATTTAGAGTTCATAAATATTAGGGTTTATTTTTCTAAATAGAATAGTTTAA 910	1849 TIATITIGICATITAGAGITCATAAANATIAGGGTITATITITCTAAATAGAATAGTITAA 1908
Best Loc Matches						Т		1
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911 ACTAAATATAACTTCAAAACGTCTAGTTTGAGTAGCTACCGTTGTTTGGAATTTT 970

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241 TGGGGATTGTGACTTGGCTGCTGTCATCCTCATGTCAAGCGCAGAAGAATCTGTGTCAG
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Pred. No. 2.8e-100;
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2988 TAACCAACATTAATAAAAGTTAAGATACCAAAACA
                                                                                                 GREERL INCOMMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dobbert, S.
APPLICANT: Globert, S.
TITLE OF INVENTION: ESTS and Encoded Human Professor File Reference: General 0.5 PR.
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
LENGTH: 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 23.6%; Score 475.6; Best Local Similarity 99.8%; Pred. No. 2.8e Matches 475; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 77.133
CHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 6.80000019073486
COTHER INFORMATION: seq AIVALAVCAALHA/SE
US-09-621-976-1513
                                                                     Sequence 1513, Application US/09621976
Patent No. 6639063
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; Sequence 7, Application US/09146580A
; Patent No. 6306653
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                     LOCATION: 77..457
NAME/KEY: sig_peptide
LOCATION: 77..133
                                             RESULT 2
US-09-621-976-1513
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NAME/KEY: CDS
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 CAGITCTTGGAGCAGCACTAGTTAGGGGCCCCAGAGTTCGGCCCTTCTGTGTGGTGATTTTA
                                               CTGATACTGAAAAAAGAAAAAGCCTGCCTTTCTGCCCAGAACCTTTTGCCTCCCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 AAGCCATACTICCCATIGCCICCAGCIGITGCACGGAGGITICACAICATAITICCAGAA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AAGCCATACTTCCCATTGCCTCCAGCTGTGCACGAGGTTTCACATCATATTTCCAGAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCTGTCATCCTTCATGTCAAGCGCAGAAGAATCTGTGTCAGCCCGCACACAACCATACTG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTAAGCAGTGGATGAAAGTGCAAGCTGCCAAGAAAATGGTAAAGGAAATGTTTGCCACA 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCTCCTGGAAAGAGTGAATATGTGTCGCATCCAGAGAGCTGATGGGGATTGTGACTTGG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCTCCTGGAAAGAGTGAATATGTGTCGCATCCAGAGAGCTGATGGGGATTGTGACTTGG 180
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APPLICANT: Papsidero, Lawrence D
APPLICANT: Dyster, Lyn M
APPLICANT: Dyster, Lyn M
APPLICANT: Frustaci, Jana M
ITLE OF INVENTION: DPECTION AND TREATMENT OF BREAST DISEASE
FILE REFERENCE: 200755/1002
CURRENT APPLICATION NUMBER: US/09/146,580A
CURRENT FILING DATE: 1998-09-03
EARLIER APPLICATION NUMBER: 60/071,889
EARLIER APPLICATION NUMBER: 60/092,155
EARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE PATENTION NUMBER: 60/092,155
EARLIER FILING DATE: 1998-07-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE PATENTION NUMBER: 60/092,155
FARLIER PATENTION NUMBER: 60/092,155
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APPLICANT: Dyster, Lyn M
THELCANT: Frustaci, Jana M
TITLE OF INVENTION: DETECTION AND TREATMENT OF BREAST DISEASE
FILE REFERENCE: 200755/1002
CURRENT APPLICATION NUMBER: US/09/146,580A
CURRENT FILIG DATE: 1998-09-03
EARLIER APPLICATION NUMBER: 60/071,889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 379; DB 4; Length 381;
Pred. No. 4.2e-78;
0; Mismatches 2; Indels
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COTHER INFORMATION: N at position 272 is either A, US-09-146-580-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at position 207 is either A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 11, Application US/09146580A
; Patent No. 6306653
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGCCATAAAACTCCTTATT 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 ACGGCCATAAACTCCTTATT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.5%;
Matches 379; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (207)
OTHER INFORMATION: N
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
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US-09-146-580-11/c
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                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCTGTCATCCTTCATGTCAAGCGCAGAAGAATCTGTGTCAGCCCCGCACAACCATACTGT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 Techercercergerangecasananarcrereraceceasancerater 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        448 GAAGAAACACCATGGCAAGAGGAACAGTAACAGGGCACATCAGGGGAAACACGAAACATA 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAAGCAGTGGATGAAAGTGCAAGCTGCCAANAAAATGGTAAAGGAAATGTTTGCCACAG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 AGCCATACTTCCCATTGCCTCCAGCTGTTGCACGAGGTTTCACATCATATTTCCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAGCAGTGGATGAAAGTGCAAGCTGCCAAGAAAAATGGTAAAGGAAATGTTTGCCACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Length 311;
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CORRESPONDENCE ADDRESS:
ADDRESSER: KOHN & ASSOCIATES
STREET: 30500 No. 6025183thwestern Highway, Suite 410
CITY: Farmington Hills
STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ü
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Patent No. 6025183
GENERAL INFORMATION:
APPLICANT: Soreq, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Shaim

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (162)
; OTHER INFORMATION: N at position 162 is either A, US-09-146-580-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
LCCATION: (101)
OTHER INFORMATION: N at position 101 is either
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.0%; Score 302; DB 4 99.3%; Pred. No. 2e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
EARLIER FILING DATE: 1998-01-20
EARLIER APPLICATION WUMBER: 60/092,155
EARLIER FILING DATE: 1998-07-09
NUMBER OF SEQ ID NOS: 18
SEGTWARE: PATENTIN Ver. 2.0
SEQ ID NO 11
LENGTH: 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY.

ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.3
Matches 302; Conservative
                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
SOFTWARE: PatentI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGC 511
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FEATURE:

NAME/KEY:
NAME/KEY:
NAME/KEY:
NAME/KEY:
NAME/KEY:
NAME/KEY:
NOCATION: 22465..2537
OTHER INFORMATION: /function= "non-translated"
OTHER INFORMATION: /function= "non-translated"
OTHER INFORMATION: /function= "non-translated"
OTHER INFORMATION: /function= "ctranslation start:
NAME/KEY:
NAME/KEY:
NAME/KEY:
OTHER INFORMATION: /function= "(translation start:
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
NAME/KEY:
NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: promoter
LOCATION: 4089..22464
OTHER INFORMATION: /function= "ACHE Promotor"
OTHER INFORMATION: /ftandard_name= "ACHE Promotor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: desc = "Cosmid including ACHE
DESCRIPTION: promotor, ACHE gene and ARS gene"
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 7q22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRATURE:
NAME/KEY: exon
LOCATION: 27255..28007
LIDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= Experimental
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /mwmber= 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 27005..27274
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene="ACHE"
OTHER INFORMATION: /number= 4
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IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
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LOCATION: 25524..26009
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene="ACHE"
OTHER INFORMATION: /number= 3
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: MONTGOMERY, IEDE N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2391.0066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEPAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 35060 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
28008..28129
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27385..27387
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NAME/KEY:
LOCATION:
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OTHER INFORMATION: // gene= "ACHE"

OTHER INPORMATION: // number= 6

NAME/KEY: execution (34528.34895)

LOCATION: complement (34528.34895)

LOCATION: complement (34528.34895)

LOCATION: complement (34528.34895)

OTHER INFORMATION: // function= "aremite resistance of the property of the complement (34022.34896)

OTHER INFORMATION: // gene= "AR"

OTHER INFORMATION: // number= 1

NAME/KEY: exon

LOCATION: complement (3493.3391)

OTHER INFORMATION: // number= 3

PERTURE: exon

LOCATION: complement (33493.3391)

OTHER INFORMATION: // number= 4

ERATURE: exon

LOCATION: complement (33292.33408)

OTHER INFORMATION: // number= 4

DOTHER INFORMATION: // number= 5

FRATURE: exon

LOCATION: complement (32939.33991)

OTHER INFORMATION: // number= 5

FRATURE: exon

LOCATION: complement (32989.33991)

OTHER INFORMATION: // number= 5

FRATURE: exon

LOCATION: complement (32989.33991)

OTHER INFORMATION: // number= 5

FRATURE: exon

LOCATION: complement (31989.33991)

OTHER INFORMATION: // number= 6

PRATURE: exon

LOCATION: complement (31989.33991)

OTHER INFORMATION: // number= 9

NAME/KEY: exon

LOCATION: complement (31989.33991)

OTHER INFORMATION: // number= 10

LOCATION: complement (31989.33991)

OTHER INFORMATION: // number= 10

NAME/KEY: exon

LOCATION: complement (31989.33991)

OTHER INFORMATION: // number= 10

NAME/KEY: exon

LOCATION: complement (31989.33991)

OTHER INFORMATION: // number= 10

NAME/KEY: exon

LOCATION: complement (31989.33991)

OTHER INFORMATION: // number= 10

PEATURE: RECOMMATION: // number= 11

PEATURE: RECOMMATION: // number= 12

NAME/KEY: exon

LOCATION: complement (31994.32080)

OTHER INFORMATION: // number= 12

NAME/KEY: exon

LOCATION: complement (31994.32080)

OTHER INFORMATION: // number= 12

NAME/KEY: exon

LOCATION: complement (31904.32080)

OTHER INFORMATION: // number= 12

NAME/KEY: exon

LOCATION: complement (30906.31011)

OTHER INFORMATION: // number= 12

NAME/KEY: exon

LOCATION: complement (30906.31011)

OTHER INFORMATION: // number= 12

NAME/KEY: exon
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GENERAL INFORMATION:
APPLICANT: Kenneth W. Dobie
APPLICANT: Mark P. Roach
TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR ALPHA EXPRESSION
FILE REFERENCE: RTS-0340
CURRENT FILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 11
LENGTH: 392000
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36753 GACCTCAGGIGATTCACCCGCCTGGGCCTTCCAAAATGCTGGGATTACAGGCGTGAGCCT 36812
                                                                                                                                                                                                           Sequence 3, Application US/09810347

Betent No. 6461847

Betent No. 6461847

GENERAL INFORMATION:

TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/810,347

CURRENT FILING DATE: 2001-03-19

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FASELSEQ for Mindows Version 4.0
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  1149 TITITGITGITGITIGGITGITITITITITGAGACAGAGICICACTCTGITGCCCAGGCTG 1208
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Pred. No. 8.3e-42;
0; Mismatches 50
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; Sequence 11, Application US/10027983
; Patent No. 6617162
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83.9%;
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Best Local Similarity 83.9
Matches 265; Conservative
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                                                                                                           7363
                                                                   TT 1509
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US-09-810-347-3
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US-09-810-347-3
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                                                                                                                                                                                                                                    LOCATION: complement (29664..29856)
OTHER INFORMATION: /gene= "ARS"
OTHER INFORMATION: /number= 16
                                                                                                                          complement (29945..30073)
IMATION: /gene= "AR"
IMATION: /number= 15
                    (30187..30274)
                                        /gene= "AR"
/number= 14
                        complement
                                   OTHER INFORMATION: //
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FEATURE:
NAME/KEY: exon
LOCATION: complement
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Sequence 3, Application US/09820005

Sequence 3, Application US/09820005

Sequence 3, Application US/09820005

GENERAL INFORMATION:

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

CURRENT APPLICATION NUMBER: US/09/820,005

CURRENT FILING DATE: 2001-03-29 1241 CCTCCGCCTCCCGCGTTCAAGTGATTCTCTTGCCTCAGCCTCCCAAGTAACTGATATTAC 1300 1301 AGCCCCCACCACCACCACCCCGCTGATTTTTGTATTTTTAGTAGACGGGTTTTCCC 1360 -1 1361 ACGITGGCCGGGCTGGTCTCAAACTCTTGACCTCAAGTGAACCACCGGCTGTGCCTCCC 1420 1181 ACAGAGTCTCACTCTGTTGCCCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCATTGCAA 67723 ACAGAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCTCAATGCCGGCTCACTGCAA 67663 CCTTCGCCTCCAGGGTTCAAGCGATTCTTGTGCCTCAGCCTCCCGAGTAGCTGGGATTAC 67484 AAAGIGCIGGGALTACAGGCGIGAGCCALCACGCCCGGCCCALTLAALTITALT 67431 1; Gaps Gaps 1421 AAAGTGCTGGAATTACCAGCGTGAGCCACCATGCCGGGCTCACACGTTTGAGTT 1474 Length 392000; 10.9%; Score 220.4; DB 4; Length 18853; 81.2%; Pred. No. 4.3e-41; Live 0; Mismatches 61; Indels 1; 11.1%; Score 223.6; DB 4; Length 78.8%; Pred. No. 2.1e-41; Live 0; Mismatches 74; Indels NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
ELEGTH: 18853
TYPE: DNA
ORGANISM: Human NAME/KEY: exon:intron junction
| LOCATION: (151129) ... (151130)
| COTHER INFORMATION: exon 5:intron 5
| NAME/KEY: exon:intron junction
| LOCATION: (299248) ... (299249)
| OTHER INFORMATION: exon 9:intron 9
| NAME/KEY: exon:intron junction
| LOCATION: (348578) ... (348579)
| OTHER INFORMATION: exon 10:intron 10
| NAME/KEY: intron
| LOCATION: (348579) ... (3181338)
| OTHER INFORMATION: intron 10
| NAME/KEY: intron:exon junction
| LOCATION: (348579) ... (381838)
| OTHER INFORMATION: intron 10
| COTHER INFORMATION: intron 11
| US-10-027-983-11 , LUCATION: (1) ...(18853); OTHER INFORMATION: n = A,T,C or GUS-09-820-005-3 Query Match
Best Local Similarity 78.8
Matches 279; Conservative Query Match 10.9 Best Local Similarity 81.2 Matches 268; Conservative NAME/KEY: misc feature LOCATION: (1) ... (18853) q à à g à g ò g ò 셤 ð 셤

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Sequence 1, Application US/09491356C
BARENAL INCORRATION:
APPLICANT: Philibert, Robert A.
APPLICANT: Shinns, Edward I.
APPLICANT: Oblist, Lynn
TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
FILE REPERRNCE: 9465.6W1S1
CURRENT APPLICATION NUMBER: US/09/491,356C
CURRENT FILING DATE: 2000-01-26
1384 CTCTTGACCTCAAGTGAACCACCGGCCTGTGCCTCCCAAAGTGCTGGAATTACCAGGGGTG 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1143 TTGTATTTTTAGTAGAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCCAACTCCTGG 1084
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                               264 CTCCTGACCTCAGGTGATCCACCTGCCTCCAAAGTGTTGGAATTACAGGTGTG 205
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                                                                                                                                                                                                                                                   Sequence 1, Application US/09584568C

Batent No. 6500657

GENERAL INFORMATION:

APPLICANT Glucksmann, Maria, Alexandra et al.

TITLE OF INVENTION: 33167, A NOVEL HUMAN HYDROLASE AND USES THEREFOR TITLE OF INVENTION: WHERE US/09/584,568C

CURRENT APPLICATION NUMBER: US/09/584,568C

CURRENT FILING DATE: 2000-05-31

PRIOR PRILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 11
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llarity 84.1%; Pred. No. 2e-41;
Conservative 0; Mismatches 48;
                                                                                       1444 AGCCACCATGCCGGGCTCACACGTT 1468
                                                                                                                                   204 AGCCACGCACCAGGCCTACTTT 180
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SEQ ID NO 1
LENGTH: 1332
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; LOCATION: (47)..(991)
US-09-584-568C-1
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Matches 260; Conserv
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Sequence 16, Application US/09183266A

GENERAL INFORMATION:
APPLICANT: Stillman, Bruce
APPLICANT: Williams, R. Sanders
APPLICANT: Milliams, R. Sanders
APPLICANT: Mendez, Juan
ITLE OF INVENTION: DANTIBODIES THERETO AND DIAGNOSTIC APPLICATIONS THEREOF
FILE REPERRORE: CSHL96-01A3
CURRENT APPLICATION NUMBER: US/09/183,266A

CURRENT PILING DATE: 1998-10-30

PRIOR APPLICATION NUMBER: 08/648,650

PRIOR PELING DATE: 1996-05-02

PRIOR PELING DATE: 1996-05-02

PRIOR PELING DATE: 1996-05-02

PRIOR APPLICATION NUMBER: 08/643,034

PRIOR FILING DATE: 1996-05-02

NUMBER OF SEQ ID NOS: 50

SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 1.6e-41;
0; Mismatches 58;
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al Similarity 81.8%;
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                                                                                                                                                   Sequence 1, Application US/09883096

Fatent No. 6880369

FighERAL INFORMATION:

APPLICANT: Beraud, Christophe

APPLICANT: Yu, Ming

APPLICANT: Yu, Ming

APPLICANT: Patel, Umesh A.

APPLICANT: Davies, Katherine A.

TILE OF INVENTION: NOVEL MOTOR PROTEINS AND METHODS FOR THEIR USE

TILE REFERENCE: 202052-001410US

CURRENT APPLICATION NUMBER: US/09/883,096

CURRENT FILING DATE: 2001-06-15

FRIOR FILING DATE: 2000-06-15

NUMBER OF SEQ ID NOS: 6

SOFTWARE PATENTION VER. 2.2.1
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OTHER INFORMATION: Description of Artificial Sequence: HsKipja gene. US-09-883-096-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 4108;
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Patent No. 6165737
GENERAL INFORMATION:
APPLICANT: Wang Xiaodong
APPLICANT: Liu, Xuesong
TITLE OF INVENTION: DNA FRAGMENTATION FACTOR INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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US-09-061-702-1
                                                                                                      RESULT 12
US-09-883-096-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1396 AGTGAACCACCGCCTGTGCCTCCCAAAGTGCTGGAATTACCAGGGTGAGCCACCATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1156 TGTTGTTTGGTTGTTTTTTTTTGAGACAGAGTCTCACTCTGTTGCCCCAGGCTGGAGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42875 CTTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTCTCGCTCTGTCGCTCAGGCTGGAGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1216 GTGGCACAATCTCGGCTCATTGCAACCTCCGCCTCCCGCGTTCAAGTGATTCTCTTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12935 ATGGCATGATCTCGGCTCACTACAACCTCGGCTCCCCGGTTAAAGCAATTCTCCTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGCCTCCCAAGTAACTGATATTACAGGCGCCCAGCCACCACCACCCGCTGATTTTTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 219.2; DB 4; Length 55298; Pred. No. 1.1e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: (485)..(485)

GOTHER INFORMATION: n is not determined
NAME/KEY: misc_feature
NAME/KEY: misc_feature

'^ation: (838)..(838)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: n.is not determined NAME/KEY: misc feature LOCATION: (22750). (22750) OTHER INFORMATION: n.is not determined NAME/KEY: misc feature LOCATION: (22756). (22756) OTHER INFORMATION: n.is not determined NAME/KEY: misc feature LOCATION: (28519). (28519) OTHER INFORMATION: n.is not determined LOCATION: (28519). (28519). (28519). (28519). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (28510). (2
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LOCATION: (44804). (44804)
OTHER INFORMATION: n is not determined
NAME/KEY: misc_feature
LOCATION: (45002). (45002)
OTHER INFORMATION: n is not determined
LOCATION: (54049). (54049).
OTHER INFORMATION: n is not determined
PRIOR APPLICATION NUMBER: PCT/US99/09365
PRIOR FILING DATE: 1999-04-29
PRIOR APPLICATION NUMBER: 60/083,465
PRIOR FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (54226)..(54226)
OTHER INFORMATION: n is not determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (838)...(838)
OTHER INFORMATION: n is not determined NAME/VEX: misc. feature
LOCATION: (16728)...(16728)
OTHER INFORMATION: n is not determined
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76.9%;
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Matches 280; Conservative
                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1456 GGGC 1459
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US-09-491-356C-1
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                                   2199 ACTCCTGACCTCAGGTGATCTGCCCGCCTCGGTCTCCCCAAAGTGCTGGGGATTACAGGCAT 2258
         AGGCTGGAGTGCAGTGGCACAATCTCGGCTCATTGCAACCTCCGCCTCCCGCGTTCAAGT 1262
                                                                                               1263 GATTCTCTTGCCTCAGCTCCCAAGTAACTGATATTACAGGCGCCCAGCCACCACCACCCC 1322
                                                                                                                                                                                          GCTGATTTTTGTATTTTTAGTAGAGGGGTTTTCCCACGTTGGCCGGGCTGGTCTCAA 1382
                                                                                                                                                                                                                              1139 GCTAATTTTTGTATGTTTAGTAGTAACGGGGTTTCACCATGTTGGCCAGGCTGTTCTCGA 2198
                                                                                                                                                                                                                                                                                   ACTCTTGACCTCAAGTGAACCACCCGCCTGTGCCTCCCAAAGTGCCTGGAATTACCAGCGT 1442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Ward
TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
FILE REFERENCE: RTS-0205
CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Pred. No. 3.6e-40;
0; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/09791211; Patent No. 6448080; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              1443 GAGCCACCATGCCGGGC 1459
                                                                                                                                                                                                                                                                                                                                                                                                                       2259 GAGCCACTGCACCTGAC 2275
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Best Local Similarity 80.4
Matches 279; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 24962
OTHER INFORMATION: u
NAME/KEY: unsure
LOCATION: 64383
OTHER INFORMATION: u
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LOCATION: 65468
OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: unsure
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NAME/KEY: unsure
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LOCATION: 65469
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LOCATION: 89049
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                                                  2020
         1203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1780 Argeriercargecteaagrregeceaccrregeraegeacaacaagrregrrargrarcager 1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1028 AGTCAGTTCTTGGAGCAGCACTAGTTAGGGGCCCAGAGTTCGGCCTTCTGTGTGGTGATT 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1088 ----TTACGCTCTGCCTAAACAAGGAGCCTACATTTTAGCTCCTATTCCACCCTTCTC 1143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1660 TGTGAGTACCTGGTCATACGGGTCAGTAGGGATAGAATTGTCTCTGGGCTGAGGAATTC 1719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1900 GCCCAAAAGAGGIGTCATGCTTTGGGGGTACGATGTTTATACTCCGTAAAGAACATACAA 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1144 ACACGII-TITGITGITGITTGGITGITTTTTTTTGAGACAGAGTCTCACTCTGTTGCCC 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             908 TAAACTAAATATAACTTCAAAACGTCTAGTTTGAGTAGCTACCGTTGTTTGGATTGAAAT 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTTGTGATCAAATTCAGGTTTAATGTTTTTGGTTAAGAATTTCCTACGTGAATTCGTGT 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      849 ACTIATITIGICAI-TIAGAGIICAIAAAIAITAGGGIITAITITICIAAAIAGAATAGIT 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1600 TCTTATACCTTCTGACAGCCCAACTTCCAGAGGACAGCTCTGGGGGTACTCGTTGGATGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            669 GCGCTATGCAAAIGTAGCCAATAATATACTCAAAACTCCTGGGCTCAAGCGATCCTCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTAGCCTCCCAAAGTACTGGGATTATAGGTGTGAGCCACAGTGCCTGGCCTAATTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%; Score 218.2; DB 3; Length 58.0%; Pred. No. 7.4e-41; cive 0; Mismatches 328; Indels
                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/061,702
FILING DATE: Concurrently Herewith
CLASSIFICATION:
NAME: MCMillian, Nabeela R.
REGISTRATION:
NAME: MCMillian, Nabeela R.
REGISTRATION NUMBER: D-43,363
REPERBENCE/DOCKET NUMBER: UTSD:546
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                ADDRESSE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston STATE: TX
    APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2839 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (512)474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 58.0
Matches 462; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                     NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                              USA
                                                                                                                                                           COUNTRY:
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TCAAACTCTTGACCTCAAGTGAACCACCGCCTGTGCCTCCCAAAGTGCTTGGAATTACCA 1438
                                                                                                        1918 TCGAACTCCTGACCTCAGGTGATCCTGCTGCTGCATCGACCTCCCAAGGTACTGGGATTACAG 1977
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                                                                                                                                                                  GCGTGAGCCACCATGCCGGCCTCACACGTTGAGTTGATACCATTGTGCCATTCCTTTT
1319 CCCCGCTGATTTTTGTATTTTAGTAGAGACGGGGTTTTCCCACGTTGGCCGGGCTGGTC
                       1858 CCCAGCTAATTTTTTTTTTTAGTAGACAGGGTTTCACCATGTTGGCCAGCTTGGTC
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he : 150 secs
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Job time
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                                  82285 TIGCCCAGGCIGGAGIGGAAIGGCACAAICTCGGCICACTGCAACCTCCACCTCCCGAGI 82226
                                                                                                          82225 TCAAGCAATTCCCCTGCCTCAGCTCCCCAAGTAGCTGGGATTACAGGC-ACCTGCCACCA 82167
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  TTGCCCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCATTGCAACCTCCGGCCTCCCGCGT 1256
                                                                                                                                                                                                                                                     TCTCAAACTCTTGACCTCAAGTGAACCACCCCCTGTGCCTCCCAAAGTGCTGGAATTAC 1436
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                                                                                                                                                                                            CACCCCCCTGATTTTTGTATTTTTAGTAGACGGGTTTTTCCCCACGTTGGCCGGGCTGG
                                                                                    TCAAGTGATTCTCTTGCCTCAGCCTCCCAAGTAACTGATATTACAGGCGCCCAGCCACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 45, Application US/09167681A
Fatent No. 6265501
GENERAL INFORMATION:
APPLICANT: Weinshilboum, M.D., Richard M.
APPLICANT: Weinshilboum, M.D., Richard M.
APPLICANT: Wood, Thomas C.
APPLICANT: Otterness, Dianne M.
TITLE OF INVENTION: SULFOTTANSFERASE SEQUENCE VARIANTS
FILE REFERENCE: 07039/118001
CURRENT APPLICATION NUMBER: US/09/167,681A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 52
COFFWARE: FASTSEQ for Windows Version 3.0
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NAME/KEY: CDS
LOCATION: (6543) ... (6638)
NAME/KEY: CDS
LOCATION: (7137) ... (7316)
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; LOCATION: (7439)...(7553)
US-09-167-681-45
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NAME/KEY: CDS
LOCATION: (4361)...(4507)
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LENGTH: 8447
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us-09-813-492-1.rnpb

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

July 10, 2004, 11:37:10; Search time 902 Seconds (without alignments) 10898.695 Million cell updates/sec Run on:

US-09-813-492-1 2017

Perfect score: Sequence:

Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table:

3183909 segs, 2436941669 residues Searched:

6367818 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database

Published Applications NA:\*

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| cgn2\_6/ptodata/1/pubpna/USO6\_NEW\_PUB.seq:\*
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| cgn2\_6/ptodata/1/pubpna/USO8\_PUBCOMB.seq:\*
| cgn2\_6/ptodata/1/pubpna/USO9\_PUBCOMB.seq:\*
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| cgn2\_6/ptodata/1/pubpna/USO9\_NEW\_PUB.seq:\*
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| cgn2\_6/ptodata/1/pubpna/USO9\_NEW\_PUB.seq:\*
| cgn2\_6/ptodata/1/pubpna/USO0\_NEW\_PUB.seq:\*
| cgn2\_6/ptodata/1/pubpna/USO0\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	Sequence 1. Appli	Sequence 6, Appli	Segmence 6. Appli	Sequence 1194. Ap	Segmence 255. App	Segmence 5. Appli	Sequence 1. Appli	Segmence 1. Appli	Sequence 21771 A	Segmence 3. Appli	Sequence 56. Appl	Seguence 175. App	Sequence 4899. An	Sequence 35876, A
	£.		US-09-813-492-1	US-09-834-795A-6	US-09-834-794A-6	US-10-106-698-1194	US-10-296-115-255	US-09-898-751A-5	US-10-146-496-1	US-09-931-381A-1	US-09-814-353-21771	US-10-146-496-3	US-09-964-824A-56	US-09-873-367C-175	US-10-029-386-4899	US-09-918-995-35876
			σ	σ	10	15	13	σ	15	σ	10	15	6	10	15	10
	Query		2017	3117	3117	643	698	731	731	768	904	496	472	472	533	411
ф	Query		100.0	51.3	51.3	26.9	24.9	24.7	24.7	24.6	20.8	18.3	17.9	17.9	17.7	17.6
	97000		2017	1035.2	1035.2	542.2	501.8	498	498	497	418.6	369.6	361.8	361.8	356.4	354.8
	Result		H	2	m	4	2	9	7	80	6	10	c 11	c 12	c 13	14

Sequence 11, Appl Sequence 11, Appl Sequence 18453, A Sequence 18453, A Sequence 179, App Sequence 179, App Sequence 179, App Sequence 170, App Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 1845, App Sequence 1845, App Sequence 1945, App Sequence 1945, App Sequence 1943, App Sequence 1943, App Sequence 1944, App Sequence 1944, App Sequence 1944, App Sequence 1944, App Sequence 11, Appl Se	Sequence 599, App Sequence 71, Appl
US-09-834-795A-1 US-09-834-794A-1 US-09-814-350-4 US-10-087-192-1 US-10-087-192-1 US-10-087-192-1 US-10-087-192-1 US-10-322-281-1 US-10-322-281-1 US-10-322-281-1 US-10-322-281-1 US-10-322-281-1 US-10-322-281-1 US-10-232-281-1 US-10-232-281-1 US-10-232-281-1 US-10-232-281-1 US-10-232-281-1 US-10-232-281-1 US-10-232-281-1 US-10-232-281-1 US-10-232-281-1 US-10-232-281-1 US-09-764-869-19 US-10-21-574-1 US-09-764-869-19 US-10-21-577-1 US-09-764-869-19 US-10-21-577-1 US-09-764-869-19 US-10-21-577-1 US-09-764-869-19 US-10-21-273-1 US-09-764-869-19 US-10-21-273-1	US-09-764-860-599 US-09-764-904-71
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## ALIGNMENTS

•	0;	09	120	180	240
	Gaps				
	2017;	CTCTGC	ACTTGTO        ACTTGTO	canaco         canaco	CAGCTG
	Length 2017; Indels 0;	CTTTTC	AGCCTC	CGCCAT	TGCCTC
	; 6 ; 0	recerra	ATCGAAC          ATCGAAC	BAGGACT	FECCEAT
INE 2 0	2017; DB No. 0; natches	GCCACC	rrccre         rrccre	AGCAGAC         AGCAGAC	CCATACT
en CHEMOKII 1813,492 sion 4.0	Score 2017; Pred. No. 0; 0; Mismatches	1	CCTCAT	GAATGC	CAGAAG
SULT 1 -09-813-492-1 -09-813-492-1 -09-813-492-1 -09-813-492-1 -09-813-492-1 -09-813-492 -0-9-813-492 -0-9-813-492 -0-9-813-492 -0-9-813-492 -0-9-813-492 -0-9-813-492 -0-9-813-492 -0-9-813-492 -0-9-813-492 -0-9-813-492 -0-9-813-492 -0-9-813-492 -0-9-813-492 -0-9-813-492-1	0	TAGATACCCTGAACACCTCCCAGGGCGGGCACCTGGCTTACTTTTCCTCTGCACTTTTCTTTC	TCTGTGCCCAAGGACACCTTTAGCCTCATTTCCTGATCGAACAGCCTCACTTGTGTTGCT 	GTCAGTGCCAGTAGGCAGGCAGGCAATGCAGCAGAGAGACTCGCCATCGTGGCCTTGGC 	TGTCTGTGCGGCCCTACATGCCTCAGAAGCCATACTTCCCCATTGCCTCCAGCTGTTGCAC
nn US/098134 735A1 .k A. Craig Step Mmesh hwMaRY GLAN 14 UMBER: US/0 2001-03-21 : 2	100.0%; 100.0%; ative	GAACAC         GAACAC	AGGACA        AGGACA	GTAGGG         GTAGGG	GCCCTA
SULT 1 -09-813-492-1 -09-813-492-1 -09-813-492-1 -09-813-492-1 -09-813-492-1 -09-813-492-1 -09-813-492-1 -00-813-492-1 -00-813-492-1 -00-813-492-1 -00-813-492-1 -00-813-492-1 -00-813-492-1 -00-813-492-1 -00-813-492-1 -00-813-492-1 -00-813-492-1 -00-813-492-1 -00-813-492-1 -00-813-492-1 -00-813-492-1 -00-813-492-1 -00-813-492-1 -00-813-492-1	Query Match Best Local Similarity 100 Matches 2017; Conservative	TAGATACCCTGAACAC                 TAGATACCCTGAACAC	GTGCCCP          GTGCCCP	AGTGCCP          AGTGCCP	CTGTGC
APP APP ORMA ORMA ORMA MAD MAD MAD BB NOVEN ENCE PPLIC PPLIC FESC FESC FESC FESC FESC FESC FESC FES	Simi 7;				
REBULT 1 US-09-813-492-1 US-09-813-492-1 Sequence 1, Applicat Sequence 1, Datent No. US2002000 GENERAL INFORMATION: APPLICANT: Labow, M APPLICANT: Bhatia, TITLE OF INVENTION: FILE REFERENCE: 123- CURRENT FILING DATE NUMBER OF SEQ ID NO. CURRENT FILING DATE NUMBER OF SEQ ID NO. SOFTWARE: FastSEQ f, SEQ ID NO 1 LENGTH: 2017 TYPE: DNA CORGANISM: HUMAN	Query Match Best Local Simi Matches 2017;	ਜ ਜ	61	121	181
RESULT 1 US-09-813-49 US-09-813-49 Patent No GENERAL II APPLICANY TITLE OF FILE REFER CURRENT I CURRENT I NUMBER OF SOFTWARER	Duery Best 1 Matche				
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1678 2687 1735 2747 1794 2807 1854 2867

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2328 TGAWITITICTATITITARIARARARGGGTTTTCCCGCNTTGGCNGGGCTGGTCTCNAAN 2387
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                                                                                       2388 TCCTTGAMCTCNAKTGAACCACCGCCTGTGCCYCCCAAANTGCTGGAATTACCANGGT
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                                                                                                                                                               GANCCACCATGCCGGGCYCACACGTTTGARTTTGANACCATTGTNCCATTCCTCTTTTGG
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JAPPLICANT: LAWARENION:
APPLICANT: LAWARENION:
APPLICANT: LAWARENION:
TITLE OF INVESTION:
FILE REFERENCE: 3380/11127-US4
CURRENT APPLICATION NUMBER: US/09/834,794A
CURRENT FILING DATE: 1998-01-09
PRIOR APPLICATION NUMBER: 60/071,899
PRIOR APPLICATION NUMBER: 60/071,899
PRIOR PILING DATE: 1998-01-20
PRIOR FILING DATE: 1998-01-20
PRIOR FILING DATE: 1998-07-09
NUMBER: PARIOR PILING DATE: 1998-07-09
NUMBER: PARIOR FILING SAG ID NOS: 35
SOFTWARE: PARENTIN VERSION 3.0
SOFTWARE: PARENTIN VERSION 3.0
SEQ ID NO 6
LENGTH: 3117
TYPE: DNA
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CTHER INFORMATION: r at any position in the sequence represents
US-09-834-795A-6
                                                     LOCATION: (1)...(3117)
OTHER INFORMATION: n at any position in the sequence represents
NAME/KEY: unsure
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OCHER INPORMATION: Y at an NAME/KEY: UNBUZE
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Sequence 1194, Application US/10106698

| Publication No. US20030109690A1
| Publication No. US20030109690A1
| Publication No. US20030109690A1
| Publicant Information
| APPLICANT: Ruben et al.
| TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
| PILE REFERENCE: PA005P1
| CURRENT APPLICATION NUMBER: US/10/106,698
| CURRENT APPLICATION NUMBER: US 60/15/137
| PRIOR APPLICATION NUMBER: US 60/157,137
| PRIOR FILING DATE: 1999-01-28
| PRIOR FILING DATE: 1999-11-03
| NUMBER OF SEQ ID NOS: 8664
| SOFTWARE: Patentin Ver: 3.0
| SOFTWARE: Patentin Ver: 3.0
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NAME/KEY: unsure
LOCATION: (1)..(3117)
OTHER INFORMATION: y at any position in the sequence represents
NAME/KEY: unsure
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Homo sapiens
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ORGANISM:
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APPLICANT: Hudak, Susan A.
APPLICANT: Hudak, Susan A.
APPLICANT: Homey, Bernhard
APPLICANT: Morales, Janine M.
APPLICANT: McEvoy, Leslie M.
APPLICANT: Bowman, Edward P.
APPLICANT: Bowman, Edward P.
APPLICANT: Bowman, Edward P.
APPLICANT: Tolonik, Albert
TITLE OF INVENTION: CHEMOKINE AND RECEPTOR USES; COMPOSITIONS; METHODS
FILE REFERENCE: DX0882XK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/898,751A CURRENT FILING DATE: 2001-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: US09/471,549
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-05-27
PRIOR PLICATION NUMBER: US60/136,570
PRIOR PLICATION NUMBER: US60/113,858
PRIOR FILING DATE: 1999-05-27
PRIOR FILING DATE: 1999-12-24
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SEQ ID NO 5
LENGTH: 731
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ORGANISM: Homo sapiens
FEATURE:
NAME/FEX: CDS
LOCATION: (56)...(436)
OTHER INFORMATION:
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US-10-296-115-255
Sequence 255, Application US/10296115
Sequence 255, Application US/10296115
Sequence 256, Application No. US20040053248A1
GENERAL INFORMATION:
PAPLICANT: Hyeaq Inc
TILLE OF INVENTION:
PILE REFERENCE: 784PCT
                                                                                                                                                                                                                                                   61 AGGCTTCAAGATAGATAGGTAAGAGCCCAGTAGTGTTCATAAGAAGCCAATAGAGAGGCCAG
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                                                                              DB 15; Length 643;
                                                                                                                 Indels
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Pred. No. 1.5e-116;
                                                                                                               1; Mismatches
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CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US/9/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US/9/552,317
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 1478
; LOCATION: (617)...(617); OTHER INFORMATION: n equals a, L, g, or c US-10-106-698-1194
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Best Local Similarity 99.1%;
Matches 544; Conservative
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Best Local Similarity 99.6
Matches 503; Conservative
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APPLICANT: Soto, Hortensia
APPLICANT: Liu, Ying
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TGGAAAGAGTGAATATGTGTGTGCGCATCCAGAGAGCTGATGGGGGATTGTGACTTGGCTGCTG 242
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al Similarity 100.0%; Pred. No. 3.5e-106;
498; Conservative 0; Mismatches 0;
                                                                        APPLICATION NUMBER: US/08/978,964A FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US xx/xxx,xxx ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                  NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0684K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFRAX: (650)862-9196
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
   APPLICATION NUMBER: US/10/146,496
FILING DATE: 15-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N, may be A, C, G, or T"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                  LENGTH: 731 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                         PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                               NAME/KEY: misc feature; NAME/KEY: misc feature; LOCATION: (529)...(529); OTHER INFORMATION: unknown amino; may be "A", "C", or US-09-898-751A-5
                                                                                                                                             24.7%; Score 498; DB 9; Le
100.0%; Pred. No. 3.5e-106;
ive 0; Mismatches 0;
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Hedrick, Joseph A.
Zlotnik, Albert
TILE OF INVENTION: Mammalian Chemokines
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: DNAX Research Inst
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
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; Sequence 1, Application US/10146496
; Publication No. US2003031646A1
; GENERAL INFORMATION:
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NAME/KEY: mat_peptide
LOCATION: (122)..()
                   LOCATION: (122)..()
OTHER INFORMATION:
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APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-06-25
PRIOR FILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/210,940
PRIOR APPLICATION NUMBER: US 60/210,940
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-17-21
PRIOR SEQ ID NOS: 22037
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21771
LENDER: DATE
TUDENT DATE
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Best Local Similarity 95.8%; Pred. No. 1.6e-87;
Matches 474; Conservative 0; Mismatches 14
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i LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 904

i CTHER INFORMATION: n = A,T,C or G

08-09-814-353-21771
                                                                                                                                                              ; Sequence 21771, Application US/09814353; Publication No. US20030165831A1; GENERAL INFORMATION:
                                      TGGCCATGATTGGTTGT 497
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                                                                                                                                                                                                                                ; Sequence 1, Application US/09931381A; Sequence 1, Application US/09931381A; Sequence 1, Application US/09931381A; Patent No. US20020137107A1; Patent No. US20020137107A1; Patent No. US20020137107A1; Patent No. US20020137107A1; Patent Nukel, Eric J. APPLICANT: Runkel, Eric J. APPLICANT: Runkel, Eric J. APPLICANT: Roler-Ferran, Dulce; TITLE OF INVENTION: Method for Identifying Agents Which: TITLE OF INVENTION: CRR10; TITLE OF INVENTION: CRR10; FILE REFERENCE: 1855_2010-003; CURRENT APPLICATION NUMBER: US. US. 09/638,914; PRIOR APPLICATION NUMBER: US. 09/638,914; PRIOR FILING DATE: 2000-08-15; NUMBER OF SEQ ID NOS: 24; SOFFWARE: FastSEQ for Windows Version 4.0
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513 ATAAAACTCCTTATTAGAGAGTCTACAGATAAATCTACAGAGACAATTCCTCAAGTGGAC 572
                                 423 AIAAAACTCCTIAITIAGAGAGTCTACAGAIAAAICTACAGAGACAAITCCTCAAGTGGAC 482
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                                                                                                            TIGGCCAIGAIIGGIIGI 590
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ORGANISM: Homo sapiens
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US-09-931-381A-1
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Best Local Similarity
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US-09-931-381A-1
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CATACTTCCCATTGCCTCCAGCTGTTGCAGGAGGTTTCACATATTTCCAGAAGGCT
                                                                                                                                              CTGTCATCCTTCATGTCAAGCGCAGAAGAATCTGTGTGTCAGCCCGCACAACCATACTGTTA
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Setephen
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-73
CURRENT APPLICATION NUMBER: US/09/964,824A
CURRENT APPLICATION NUMBER: US/60/236,033
PRIOR APPLICATION NUMBER: US/60/236,033
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 583
SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 56, Application US/09964824A Patent No. US20020102531A1
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OTHER INFORMATION: n=a,t,g or
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NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
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      457 CCTCAAGTGGACTTGGCCATGATTTGGTTGTAAGTTTTTATCATCTGAATTCTCCTTA-TG 515
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CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Pred. No. 3.3e-76;
0; Mismatches 70; I
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Hedrick, Joseph A.
Zlotnik, Albert
TITLE OF INVENTION: Mammalian Chemokines
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APPLICATION NUMBER: US/08/978,964A
FILING DATE: 26-NOV-1997
APPLICATION NUMBER: US xx/xxx,xxx
FILING DATE: 24-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: DNAX Research Institute
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RPPLICATION NUMBER: US/10/146,496
FILING DATE: 15-May-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                     Sequence 3, Application US/10146496
Publication No. US20030031646A1
GENERAL INFORMATION:
APPLICANT: Vicari, Alain
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TYPE: nucleic acid
STRANDEDNESS: single
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85.0%;
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CORRESPONDENCE ADDRESS:
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Best Local Similarity 85.0
Matches 420; Conservative
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US-10-146-496-3
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17.7%; Score 356.4; DB 1:
Best Local Similarity 97.1%; Pred. No. 4.3e-73;
Matches 363; Conservative 0; Mismatches 11.
                                                                                                                                                                                                                                                                      Sequence 4899, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
                                                                                                                                                  GITAAGATACCAAAAA 2008
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP T
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APPLICANT: Young, Paul
APPLICANT: Soppet, Daniel
APPLICANT: Soppet, Daniel
APPLICANT: Soppet, Daniel
APPLICANT: Budress, Gregory
APPLICANT: Budress, Gregory
APPLICANT: Augustus, Meena
APPLICANT: Carter, Reinhard
APPLICANT: Carter, Renneth
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-64
CURRENT APPLICATION NUMBER: US/09/873,367C
PRIOR APPLICATION NUMBER: US. 60/236,891
PRIOR APPLICATION NUMBER: US. 60/236,892
PRIOR APPLICATION NUMBER: US. 60/244,867
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 1067
                                                                  GTGGCAGAGACAAGCTTTTTAAATAAGAAAAATTAATAAAATATAATATATGAGAGTAACT 1931
                                                                                                                                       TAAAATATTAATAAACCACAATTTTAAATTAATTAACCGTGATAACCAACATTAATAAAA 1991
TATAGATGAGGAAATTTGAGGCTCTTAGAGGTAAAATGACTTGCCCCAGGTCACACAGGAA 1871
                            291 TATAGATGAGGAATTTTGAGGGTCTTAGAGGTAAATGACTTGCCCAGGTCACACAGGAA 232
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99.2%; Pred. No. 2.2e-74;
live 0; Mismatches 2; 1
                                                                                                                                                                                                                                                                                           RESULT 12
US-09-873-367C-175/c
; Sequence 175, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
                                                                                                                                                                                                            GTTAAGATACCAAAAA 2008
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j OTHER INFORMATION: n=a,t,g or c
US-09-873-367C-175
                                                                                                                                                                                                                                            GTTAAGATACCAAAACA 95
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Best Local Similarity 99.2
Matches 374; Conservative
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LENGTH: 472
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REPERENCE: AEOMICA.X.-2
CURRENT FILING DATE: 2001-12-20
CURRENT FILING DATE: 2001-12-20
SOFTWARRE: APPLICATION NUMBER: US/10/029,386
SOFTWARRE: APPLICATION NUMBER: US/10/029,386
SOFTWARRE: APPLICATION NUMBER: 2001-12-20
LEBOTH ST. 11
SEQ ID NO 4899
LENGHIS 333
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1932 TAAAATTTAATAAACCACAATTTTAAATTAATTAACGGGGATAACCAACATTAATAAAA
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N: EXPRESSED IN BONE MARROW, SIGNAL = 2.5

N: EXPRESSED IN BOULT LIVER, SIGNAL = 2

N: EXPRESSED IN HELA, SIGNAL = 2.7

N: EXPRESSED IN LUNG, SIGNAL = 3.8

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2

N: WISSEROT HTT: Q9NRJ3, EVALUE 7.00e-35

N: NT HIT: AF266504.1, EVALUE 0.00e+00

N: EXT_HUMAN HIT: BG530240.1, EVALUE 0.00e+00
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APPLICANT: Lawrence, Papsidero

APPLICANT: Lawrence, Papsidero

APPLICANT: Lawrence, Papsidero

TILE OF INVENTION: Detection and Treatment of Breast Cancer

TILE OF INVENTION: Detection and Treatment of Breast Cancer

TILE OF INVENTION: Detection and Treatment of Breast Cancer

CURRENT APPLICATION UNMER: US/09/834,795A

CURRENT FILING DATE: 2001-04-12

PRIOR APPLICATION NUMBER: 09/146,580

PRIOR APPLICATION NUMBER: 60/071,899

PRIOR APPLICATION NUMBER: 60/071,899

PRIOR APPLICATION NUMBER: 60/092,155

PRIOR FILING DATE: 1998-00-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 17.6%; Score 354.8; DB 10; Length 411; Best Local Similarity 99.4%; Pred. No. 8.7e-73; Matches 356; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                 APPLICANT: Hyseq, Inc.

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

FRIOR PHILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                  Sequence 35876, Application US/09918995 Publication No. US20030073623A1 GENERAL INFORMATION:
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                                                GCAAATGTAGCCAA 1
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US-09-918-995-35876
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US-09-918-995-35876
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                                                                                                                                                                                                                                                             Length 311;
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                                                                                                                                                                                                                                                               15.0%; Score 302; DB 9;
99.3%; Pred. No. 1.7e-60;
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                                                                                                    FEATURE:

NAME/KEY: unsure

LOCATION: (101)...(101)

OTHER INFORMATION: n may be a or g or

LOCATION: (162)...(162)

GOTHER INFORMATION: n may be a or g or

US-09-834-795A-11
NUMBER OF SEQ ID NOS: 35
SOFWARE: Patentin version 3.0
SEQ ID NO 11
LENGTH: 311
                                                                                                                                                                                                                                                                                  Best Local Similarity 99.3
Matches 302, Conservative
                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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